



SEQUENCE LISTING

<110> JURIDICAL FOUNDATION THE CHEMO-SERO-THERAPEUTIC RESEARCH INSTITUTE

<120> Antibody against von Willebrand Factor cleaving protease and the assay method using the antibody thereof

<130> PH-1893-PCT

<140> US/10/529, 009

<141> 2005-03-24

<150> JP 2002/279924

<151> 2002-09-25

<150> JP 2002/377569

<151> 2002-12-26

<160> 20

<210> 1

<211> 1427

<212> PRT

<213> Homo sapiens

<400> 1

Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val

1 5 10 15

Ala Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro

20 25 30

Ser His Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala

35 40 45

Val Ser Ser Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro		
	50	55 60
Pro Ser Pro Gly Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala		
	65	70 75
Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val Ala Val Gly Pro		
	80	85 90
Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg Tyr Val Leu		
	95	100 105
Thr Asn Leu Asn Ile Gly Ala Glu Leu Leu Arg Asp Pro Ser Leu		
	110	115 120
Gly Ala Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr		
	125	130 135
Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser		
	140	145 150
Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp		
	155	160 165
Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg		
	170	175 180
Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val Arg Gly Val		
	185	190 195
Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu Ile		
	200	205 210
Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His Glu		
	215	220 225
Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser		
	230	235 240
Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala		
	245	250 255

Pro Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu		
260	265	270
Leu Ser Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro		
275	280	285
Pro Arg Pro Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln		
290	295	300
Pro Gly Leu Tyr Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe		
305	310	315
Gly Pro Lys Ala Val Ala Cys Thr Phe Ala Arg Glu His Leu Asp		
320	325	330
Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln Ser		
335	340	345
Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys		
350	355	360
Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val		
365	370	375
Glu Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp		
380	385	390
Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val		
395	400	405
Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly		
410	415	420
Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr		
425	430	435
Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln Gln Cys		
440	445	450
Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly Ala		
455	460	465

Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp		
	470	475 480
Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile		
	485	490 495
Met Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro		
	500	505 510
Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly		
	515	520 525
Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln		
	530	535 540
Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys		
	545	550 555
Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr		
	560	565 570
Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr Ile		
	575	580 585
Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly		
	590	595 600
Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr		
	605	610 615
Thr Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val		
	620	625 630
Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile		
	635	640 645
Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln Val Tyr Arg Arg		
	650	655 660
Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp Ile Thr Phe		
	665	670 675

Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp Ala Ala	680	685	690
Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg Trp	695	700	705
Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu	710	715	720
Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu	725	730	735
Ala Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp	740	745	750
Phe Gly Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg	755	760	765
Pro Val Arg Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu	770	775	780
Pro Pro Ala Arg Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala	785	790	795
Leu Glu Thr Cys Asn Pro Gln Pro Cys Pro Ala Arg Trp Glu Val	800	805	810
Ser Glu Pro Ser Ser Cys Thr Ser Ala Gly Gly Ala Gly Leu Ala	815	820	825
Leu Glu Asn Glu Thr Cys Val Pro Gly Ala Asp Gly Leu Glu Ala	830	835	840
Pro Val Thr Glu Gly Pro Gly Ser Val Asp Glu Lys Leu Pro Ala	845	850	855
Pro Glu Pro Cys Val Gly Met Ser Cys Pro Pro Gly Trp Gly His	860	865	870
Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala Pro Ser Pro Trp Gly	875	880	885

Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp Thr Pro Ala			
	890	895	900
Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu Met Glu Leu			
	905	910	915
Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val Gln Glu			
	920	925	930
Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu Val			
	935	940	945
Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala			
	950	955	960
Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu			
	965	970	975
Tyr Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu			
	980	985	990
Leu Asp Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu			
	995	1000	1005
Ala Cys Ser Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser			
	1010	1015	1020
Leu Gly Pro Cys Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg			
	1025	1030	1035
Ser Val Ala Cys Val Gln Leu Asp Gln Gly Gln Asp Val Glu Val			
	1040	1045	1050
Asp Glu Ala Ala Cys Ala Ala Leu Val Arg Pro Glu Ala Ser Val			
	1055	1060	1065
Pro Cys Leu Ile Ala Asp Cys Thr Tyr Arg Trp His Val Gly Thr			
	1070	1075	1080
Trp Met Glu Cys Ser Val Ser Cys Gly Asp Gly Ile Gln Arg Arg			
	1085	1090	1095

Arg Asp Thr Cys Leu Gly Pro Gln Ala Gln Ala Pro Val Pro Ala			
1100	1105	1110	
Asp Phe Cys Gln His Leu Pro Lys Pro Val Thr Val Arg Gly Cys			
1115	1120	1125	
Trp Ala Gly Pro Cys Val Gly Gln Gly Thr Pro Ser Leu Val Pro			
1130	1135	1140	
His Glu Glu Ala Ala Ala Pro Gly Arg Thr Thr Ala Thr Pro Ala			
1145	1150	1155	
Gly Ala Ser Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu Phe Ser			
1160	1165	1170	
Pro Ala Pro Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu Asn			
1175	1180	1185	
Ser Val Gln Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr			
1190	1195	1200	
Gly Thr Ile Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val			
1205	1210	1215	
Ala Ile Gly Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu			
1220	1225	1230	
Glu Ser Ser Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp			
1235	1240	1245	
Gly Arg Leu Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met			
1250	1255	1260	
Thr Phe Ser Ser Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys			
1265	1270	1275	
Gly Arg Pro Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu			
1280	1285	1290	
Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe Gly			
1295	1300	1305	

Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser			
	1310	1315	1320
Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala			
	1325	1330	1335
Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr			
	1340	1345	1350
Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser			
	1355	1360	1365
Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu			
	1370	1375	1380
Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu			
	1385	1390	1395
Lys Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser			
	1400	1405	1410
Trp Val Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu			
	1415	1420	1425
Gly Thr			

<210>2

<211>22

<212>PRT

<213>Homo sapiens

<400>2

Phe Ser Pro Ala Pro Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln			
1	5	10	15
Glu Asn Ser Val Gln Ser Ser			
	20		

<210>3

<211>18

<212>PRT

<213>Homo sapiens

<400>3

Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro Leu

1 5 10 15

Gln Glu Asp

<210>4

<211>30

<212>DNA

<213>Homo sapiens

<400>4

ctggagcacg acggcgcgcc cggcagcggc 30

<210>5

<211>30

<212>DNA

<213>Homo sapiens

<400>5

atgtgcaaca ctcaggcctg cgagaagacc 30

<210>6

<211>30

<212>DNA

<213>Homo sapiens

<400>6

ccaacctgac cagtgtctac attgccaacc

30

<210>7

<211>21

<212>DNA

<213>Homo sapiens

<400>7

ctggagccct gccacctag g

21

<210>8

<211>62

<212>DNA

<213>Homo sapiens

<400>8

tccgtcgact cttatcactt atcgtcatcg tccttgtagt cgtcccacac gcagcgcgcc 60

cg 62

<210>9

<211>62

<212>DNA

<213>Homo sapiens

<400>9

tccgtcgact cttatcactt atcgtcatcg tccttgtagt cgcgcccattg cactgctgct 60

at 62

<210>10

<211>62

<212>DNA

<213>Homo sapiens

<400>10

gccgtcgact cttatcactt atcgtcacg tcctttagt ctgcgacat gaactccagc	60
tg	62

<210>11

<211>62

<212>DNA

<213>Homo sapiens

<400>11

gccgtcgact cttatcactt atcgtcacg tcctttagt ccaggttggg ggtaactgtc	60
ag	62

<210>12

<211>62

<212>DNA

<213>Homo sapiens

<400>12

tccgtcgact cttatcactt atcgtcacg tcctttagt ccacccaggc ctgccgtggc	60
tt	62

<210>13

<211>62

<212>DNA

<213>Homo sapiens

<400>13

tccgtcgact cttatcactt atcgtcacg tcctttagt cgtagggagg gcagggttcg	60
ag	62

<210>14

<211>62

<212>DNA

<213>Homo sapiens

<400>14

tccgtcgact cttatcactt atcgtcacg tccttgtagt ccctggcagg gcagggctgg 60
gg 62

<210>15

<211>62

<212>DNA

<213>Homo sapiens

<400>15

gccgtcgact cttatcactt atcgtcacg tccttgtagt ccacgtgtgc agcttgagcc 60
cc 62

<210>16

<211>62

<212>DNA

<213>Homo sapiens

<400>16

gccgtcgact cttatcactt atcgtcacg tccttgtagt ccctaggtgg gcagggctcc 60
ag 62

<210>17

<211>62

<212>DNA

<213>Homo sapiens

<400>17

gccgtcgact cttatcactt atcgatcatg tcctttagt caccctgtcc cacacagggc 60
cc 62

<210>18

<211>60

<212>DNA

<213>Homo sapiens

<400>18

tccaagcttg tcgactctta tcacttatcg tcacgtcct ttagtcggg tccttccttt 60

<210>19

<211>27

<212>DNA

<213>Artificial Sequence

<220>

<223>Description of Artificial Sequence:Synthetic DNA

<400>19

gactacaagg acgatgacga taagtga 27

<210>20

<211>8

<212>PRT

<213>Artificial Sequence

<220>

<223>Description of Artificial Sequence:Synthetic

<400>20

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5